RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/884, 901 A_

Source: _IFW16_

Date Processed by STIC: _09/22/2005_

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RAW SEQUENCE LISTING   DATE: 09/22/2005
PATENT APPLICATION: US/09/884,901A   TIME: 09:55:14

Input Set : **A:\UOFW17396seq.txt**
Output Set: **N:\CRF4\09222005\I884901A.raw**

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  3 <110> APPLICANT: Miao, Carol
  4        Kay, Mark
  6 <120> TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
  8 <130> FILE REFERENCE: UOFW-1-17396
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/884,901A
C--> 10 <141> CURRENT FILING DATE: 2001-06-18
 10 <150> PRIOR APPLICATION NUMBER: US 60/212,902
 11 <151> PRIOR FILING DATE: 2000-06-20
 13 <160> NUMBER OF SEQ ID NOS: 18
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1438
 19 <212> TYPE: DNA
 20 <213> ORGANISM: HomoSapien
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 25 atgctgtctt cttcactaaa ttttgattac atgatttgac agcaatattg aagagtctaa       120
 27 cagccagcac gcaggttggt aagtactggt tctttgttag ctaggttttc ttcttcttca       180
 29 tttttaaaac taaatagatc gacaatgctt atgatgcatt tatgtttaat aaacactgtt       240
 31 cagttcatga tttggtcatg taattcctgt tagaaaacat tcatctcctt ggtttaaaaa       300
 33 aattaaaagt gggaaaacaa agaaatagca gaatatagtg aaaaaaaata accacattat       360
 35 ttttgtttgg acttaccact ttgaaatcaa aatgggaaac aaaagcacaa acaatggcct       420
 37 tatttacaca aaaagtctga ttttaagata tatgacattt caaggtttca gaagtatgta       480
 39 atgaggtgtg tctctaattt tttaaattat atatcttcaa tttaaagttt tagttaaaac       540
 41 ataaagatta accttttcatt agcaagctgt tagttatcac caaagctttt catggattag      600
 43 gaaaaaatca ttttgtctct atgtcaaaca tcttggagtt gatatttggg gaaacacaat       660
 45 actcagttga gttccctagg ggagaaaagc aagcttaaga attgacataa agagtaggaa       720
 47 gttagctaat gcaacatata tcactttgtt ttttcacaac tacagtgact ttatgtattt       780
 49 cccagaggaa ggcatacagg gaagaaatta tcccatttgg acaaacagca tgttctcaca       840
 51 ggaagcattt atcacactta cttgtcaact ttctagaatc aaatctagta gctgacagta       900
 53 ccaggatcag gggtgccaac cctaagcacc cccagaaagc tgactggccc tgtggttccc       960
 55 actccagaca tgatgtcagc tgtgaaatcg acgtcgctgg accataatta ggcttctgtt      1020
 57 cttcaggaga catttgttca aagtcatttg ggcaaccata ttctgaaaac agcccagcca      1080
 59 gggtgatgga tcactttgca aagatcctca atgagctatt ttcaagtgat gacaaagtgt      1140
 61 gaagttaacc gctcatttga gaactttctt tttcatccaa agtaaattca aatatgatta      1200
 63 gaaatctgac cttttattac tggaattctc ttgactaaaa gtaaaattga attttaattc      1260
 65 ctaaatctcc atgtgtatac agtactgtgg gaacatcaca gattttggct ccatgcccta      1320
 67 aagagaaatt ggctttcaga ttatttggat taaaaacaaa gactttctta agagatgtaa      1380
 69 aattttcatg atgttttctt ttttgctaaa actaagaat tattctttta catttcag        1438
 72 <210> SEQ ID NO: 2
 73 <211> LENGTH: 1413
 74 <212> TYPE: DNA
 75 <213> ORGANISM: HomoSapien
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78 <221> NAME/KEY: CDS
79 <222> LOCATION: (30)..(1412)
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83                                   Met Gln Arg Val Asn Met Ile Met
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86 gca gaa tca cca ggc ctc atc acc atc tgc ctt tta gga tat cta ctc      101
87 Ala Glu Ser Pro Gly Leu Ile Thr Ile Cys Leu Leu Gly Tyr Leu Leu
88     10              15              20
90 agt gct gaa tgt aca gtt ttt ctt gat cat gaa aac gcc aac aaa att      149
91 Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala Asn Lys Ile
92 25              30                  35                  40
94 ctg aat cgg cca aag agg tat aat tca ggt aaa ttg gaa gag ttt gtt      197
95 Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val
96                 45              50                  55
98 caa ggg aac ctt gag aga gaa tgt atg gaa gaa aag tgt agt ttt gaa      245
99 Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu
100             60                  65                  70
102 gaa gca cga gaa gtt ttt gaa aac act gaa aga aca act gaa ttt tgg     293
103 Glu Ala Arg Glu Val Phe Glu Asn Thr Glu Arg Thr Thr Glu Phe Trp
104             75                  80                  85
106 aag cag tat gtt gat gga gat cag tgt gag tcc aat cca tgt tta aat     341
107 Lys Gln Tyr Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn
108     90                  95                  100
110 ggc ggc agt tgc aag gat gac att aat tcc tat gaa tgt tgg tgt ccc     389
111 Gly Gly Ser Cys Lys Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro
112 105   ·             110                 115                 120
114 ttt gga ttt gaa gga aag aac tgt gaa tta gat gta aca tgt aac att     437
115 Phe Gly Phe Glu Gly Lys Asn Cys Glu Leu Asp Val Thr Cys Asn Ile
116                 125                 130                 135
118 aag aat ggc aga tgc gag cag ttt tgt aaa aat agt gct gat aac aag     485
119 Lys Asn Gly Arg Cys Glu Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys
120             140                 145                 150
122 gtg gtt tgc tcc tgt act gag gga tat cga ctt gca gaa aac cag aag     533
123 Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys
124         155                 160                 165
126 tcc tgt gaa cca gca gtg cca ttt cca tgt gga aga gtt tct gtt tca     581
127 Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser Val Ser
128     170                 175                 180
130 caa act tct aag ctc acc cgt gct gag gct gtt ttt cct gat gtg gac     629
131 Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp
132 185                 190                 195                 200
134 tat gta aat tct act gaa gct gaa acc att ttg gat aac atc act caa     677
135 Tyr Val Asn Ser Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln
136                 205                 210                 215
138 agc acc caa tca ttt aat gac ttc act cgg gtt gtt ggt gga gaa gat     725
139 Ser Thr Gln Ser Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp
140                 220                 225                 230
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142 gcc aaa cca ggt caa ttc cct tgg cag gtt gtt ttg aat ggt aaa gtt      773
143 Ala Lys Pro Gly Gln Phe Pro Trp Gln Val Val Leu Asn Gly Lys Val
144         235             240                 245
146 gat gca ttc tgt gga ggc tct atc gtt aat gaa aaa tgg att gta act      821
147 Asp Ala Phe Cys Gly Gly Ser Ile Val Asn Glu Lys Trp Ile Val Thr
148         250             255                 260
150 gct gcc cac tgt gtt gaa act ggt gtt aaa att aca gtt gtc gca ggt      869
151 Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr Val Val Ala Gly
152 265             270                 275                 280
154 gaa cat aat att gag gag aca gaa cat aca gag caa aag cga aat gtg      917
155 Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn Val
156             285                 290                 295
158 att cga att att cct cac cac aac tac aat gca gct att aat aag tac      965
159 Ile Arg Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr
160         300             305                 310
162 aac cat gac att gcc ctt ctg gaa ctg gac gaa ccc tta gtg cta aac     1013
163 Asn His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn
164         315             320                 325
166 agc tac gtt aca cct att tgc att gct gac aag gaa tac acg aac atc     1061
167 Ser Tyr Val Thr Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile
168         330             335                 340
170 ttc ctc aaa ttt gga tct ggc tat gta agt ggc tgg gga aga gtc ttc     1109
171 Phe Leu Lys Phe Gly Ser Gly Tyr Val Ser Gly Trp Gly Arg Val Phe
172 345             350                 355                 360
174 cac aaa ggg aga tca gct tta gtt ctt cag tac ctt aga gtt cca ctt     1157
175 His Lys Gly Arg Ser Ala Leu Val Leu Gln Tyr Leu Arg Val Pro Leu
176             365                 370                 375
178 gtt gac cga gcc aca tgt ctt cga tct aca aag ttc acc atc tat aac     1205
179 Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe Thr Ile Tyr Asn
180         380             385                 390
182 aac atg ttc tgt gct ggc ttc cat gaa gga ggt aga gat tca tgt caa     1253
183 Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser Cys Gln
184         395             400                 405
186 gga gat agt ggg gga ccc cat gtt act gaa gtg gaa ggg acc agt ttc     1301
187 Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe
188         410             415                 420
190 tta act gga att att agc tgg ggt gaa gag tgt gca atg aaa ggc aaa     1349
191 Leu Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys
192 425             430                 435                 440
194 tat gga ata tat acc aag gta tcc cgg tat gtc aac tgg att aag gaa     1397
195 Tyr Gly Ile Tyr Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu
196             445                 450                 455
198 aaa aca aag ctc act t                                              1413
199 Lys Thr Lys Leu Thr
200             460
203 <210> SEQ ID NO: 3
204 <211> LENGTH: 461
205 <212> TYPE: PRT
206 <213> ORGANISM: HomoSapien
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214 Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
215   20   25   30
218 Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
219   35   40   45
222 Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
223   50   55   60
226 Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
227 65   70   75   80
230 Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
231   85   90   95
234 Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
235   100   105   110
238 Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
239   115   120   125
242 Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
243   130   135   140
246 Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
247 145   150   155   160
250 Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
251   165   170   175
254 Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
255   180   185   190
258 Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu
259   195   200   205
262 Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe
263   210   215   220
266 Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
267 225   230   235   240
270 Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
271   245   250   255
274 Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
275   260   265   270
278 Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
279   275   280   285
282 His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn
283   290   295   300
286 Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu Glu
287 305   310   315   320
290 Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile
291   325   330   335
294 Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr
295   340   345   350
298 Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val
299   355   360   365
302 Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg
303   370   375   380

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306 Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His
307 385                 390                 395                 400
310 Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val
311             405                 410                 415
314 Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly
315             420                 425                 430
318 Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser
319         435                 440                 445
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323     450                 455                 460
326 <210> SEQ ID NO: 4
327 <211> LENGTH: 771
328 <212> TYPE: DNA
329 <213> ORGANISM: HomoSapien
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336 ctactcatgt ccctaaaatg ggcaaacatt gcaagcagca aacagcaaac acacagccct    180
338 ccctgcctgc tgaccttgga gctggggcag aggtcagaga cctctctggg cccatgccac    240
340 ctccaacatc cactcgaccc cttggaattt cggtggagag gagcagaggt tgtcctggcg    300
342 tggtttaggt agtgtgagag ggtccgggtt caaaaccact tgctgggtgg ggagtcgtca    360
344 gtaagtggct atgccccgac cccgaagcct gtttccccat ctgtacaatg gaaatgataa    420
346 agacgcccat ctgatagggt ttttgtggca aataaacatt tggttttttt gttttgtttt    480
348 gttttgtttt ttgagatgga ggtttgctct gtcgcccagg ctggagtgca gtgacacaat    540
350 ctcatctcac cacaaccttc ccctgcctca gcctcccaag tagctgggat tacaagcatg    600
352 tgccaccaca cctggctaat tttctatttt tagtagagac gggtttctcc atgttggtca    660
354 gcctcagcct cccaagtaac tgggattaca ggcctgtgcc accacacccg gctaattttt    720
356 tctattttg acagggacgg ggtttcacca tgttggtcag gctcctctag a              771
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360 <211> LENGTH: 418
361 <212> TYPE: DNA
362 <213> ORGANISM: HomoSapien
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369 cgctgtggtt tctgagccag gtacaatgac tcctttcggt aagtgcagtg gaagctgtac    180
371 actgcccagg caaagcgtcc gggcagcgta ggcgggcgac tcagatccca gccagtggac    240
373 ttagcccctg tttgctcctc cgataactgg ggtgaccttg gttaatattc accagcagcc    300
375 tccccgttg cccctctgga tccactgctt aaatacggac gaggacaggg ccctgtctcc    360
377 tcagcttcag gcaccaccac tgacctggga cagtgaatga tcccctgat ctgcggcc       418
380 <210> SEQ ID NO: 6
381 <211> LENGTH: 282
382 <212> TYPE: DNA
383 <213> ORGANISM: Bos taurus
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388 cccgtgcctt ccttgaccct ggaaggtgcc actcccactg tcctttccta ataaaatgag    120
390 gaaattgcat cgcattgtct gagtaggtgt cattctattc tggggggtgg ggtggggcag    180
392 gacagcaagg gggaggattg ggaagacaat agcaggcatg ctggggatgc ggtgggctct    240
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VERIFICATION SUMMARY   DATE: 09/22/2005
PATENT APPLICATION: **US/09/884,901A**   TIME: 09:55:15

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date